



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/863,049
Source: OTPE
Date Processed by STIC: 1/28/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/efc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

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Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: 09/863,049

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11 **Use of <220>** Sequence(s) 57-61 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 **Misuse of n** n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1645

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/863,049

DATE: 01/28/2002

TIME: 18:04:25

Input Set : N:\paola\09863049.txt

Output Set: N:\CRF3\01282002\I863049.raw

**Does Not Comply
Corrected Diskette Needed**

3 <110> APPLICANT: Kenwrick, Sue J.
 4 Nelson, David L.
 5 Aradhya, Swaroop
 6 D'Urso, Michele
 7 Woffendin, Hayley
 8 Munnich, Arnold
 9 Smahi, Asmae
 10 Israel, Alain
 11 Poustka, Annemarie
 12 Lewis, Richard A
 13 Levy, Moise
 14 Heiss, Nina
 16 <120> TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated
 with Defective
 17 NFKAPPA B (NF-kB) Activation
 19 <130> FILE REFERENCE: HO-P01961US1
 21 <140> CURRENT APPLICATION NUMBER: US 09/863,049
 22 <141> CURRENT FILING DATE: 2001-05-22
 24 <150> PRIOR APPLICATION NUMBER: US 60/206,223
 25 <151> PRIOR FILING DATE: 2000-05-22
 27 <160> NUMBER OF SEQ ID NOS: 77
 29 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

1719 <210> SEQ ID NO: 77
 1720 <211> LENGTH: 11
 1721 <212> TYPE: PRT
 1722 <213> ORGANISM: Human
 1724 <400> SEQUENCE: 77
 1726 Leu Gln Arg Cys Leu Glu Glu Asn Gln Glu Leu
 1727 1 5 10
 E--> 1730 25110578 - 29 -

delete

*See next page for
more errors*

090630492

<210> 57
<211> 43
<212> DNA
<213> Artificial

see item 11 on Eva Summary Sheet

<400> 57
ctaatacgac tcactatagg gctcgagcag cctccgaggg cag

↓
43
The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

FSI

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/863,049

DATE: 01/28/2002

TIME: 18:04:26

Input Set : N:\paola\09863049.txt

Output Set: N:\CRF3\01282002\I863049.raw

L:1480 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:57
 L:1482 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:1482 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:1489 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:58
 L:1491 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:1491 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:1498 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:59
 L:1500 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:1500 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:1507 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:60
 L:1509 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:1509 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:1516 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:61
 L:1518 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:1518 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:1572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
 L:1634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
 L:1730 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:77